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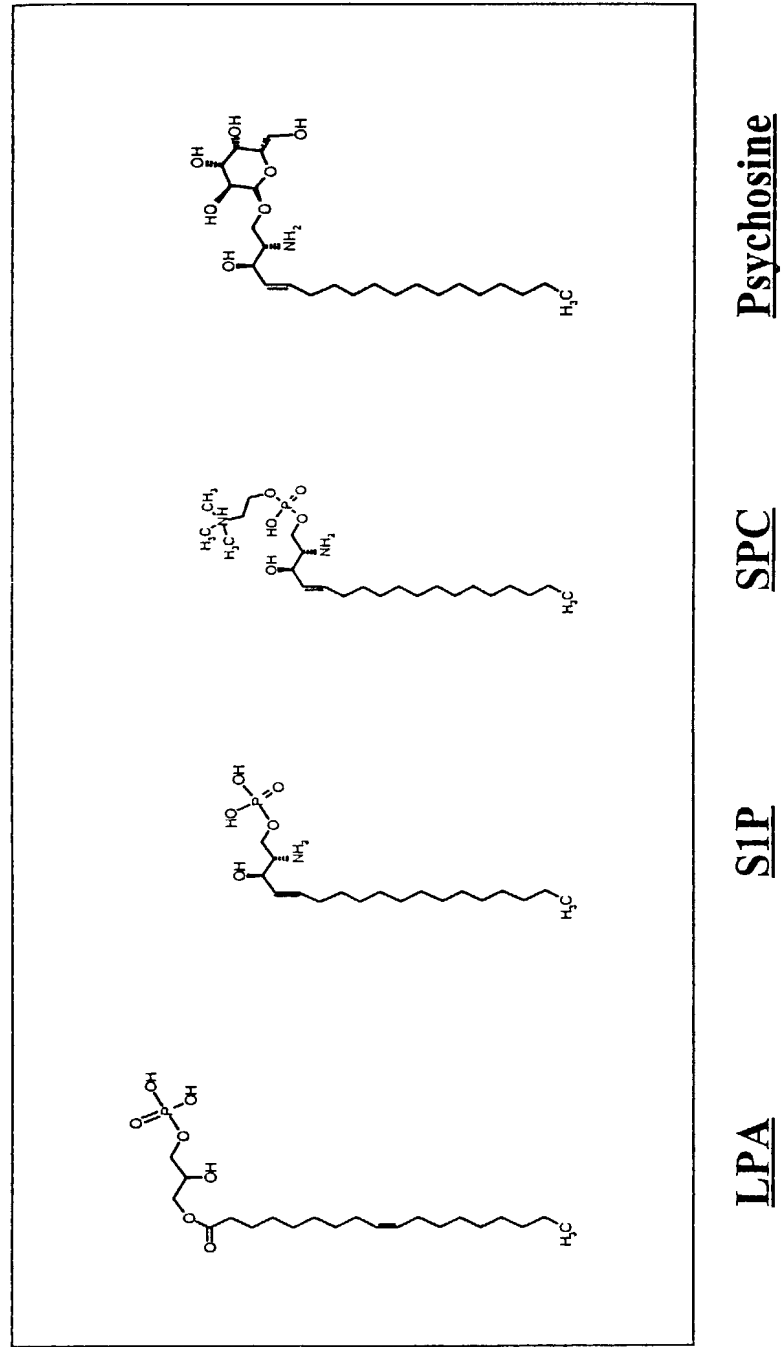


Figure 1B.

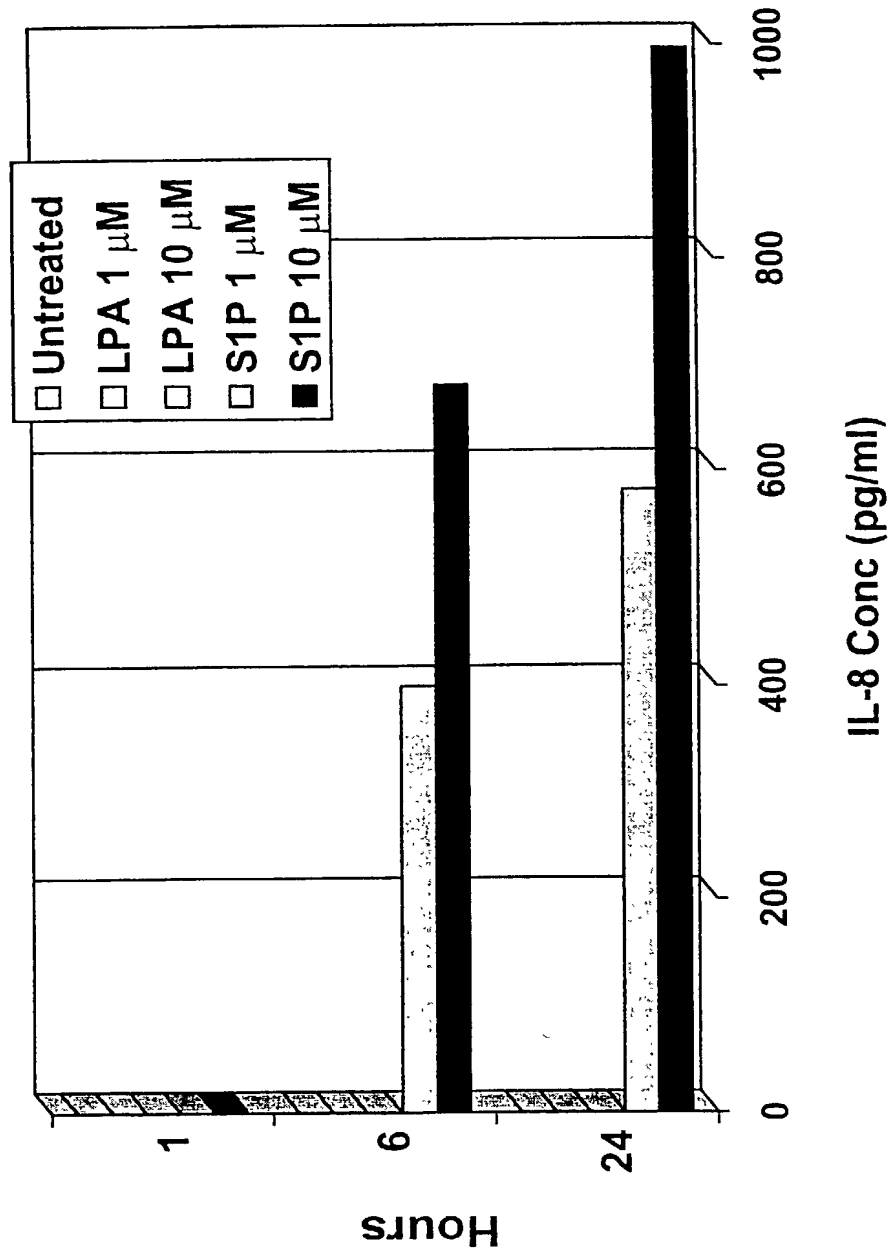


Figure 2A.

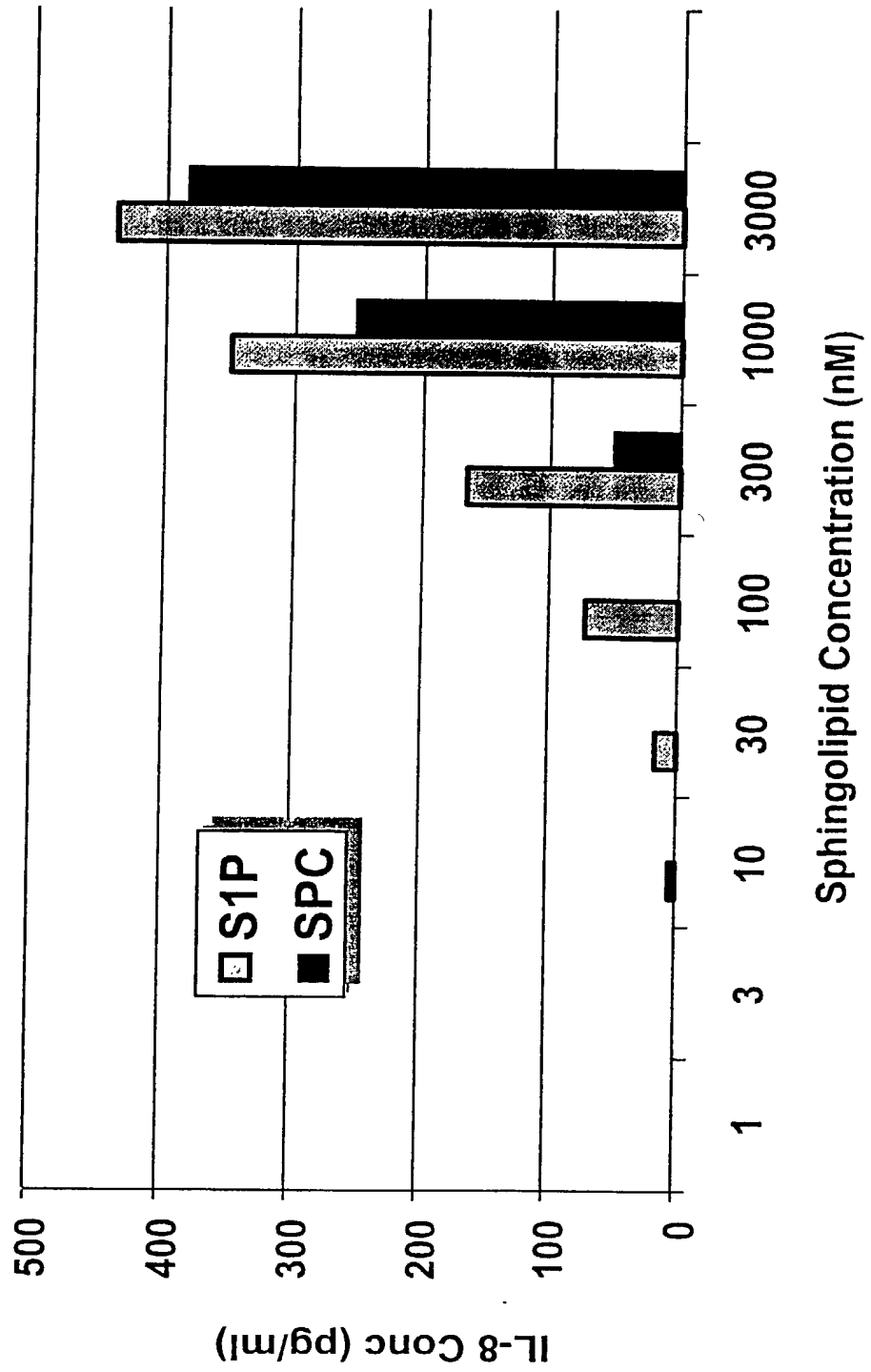
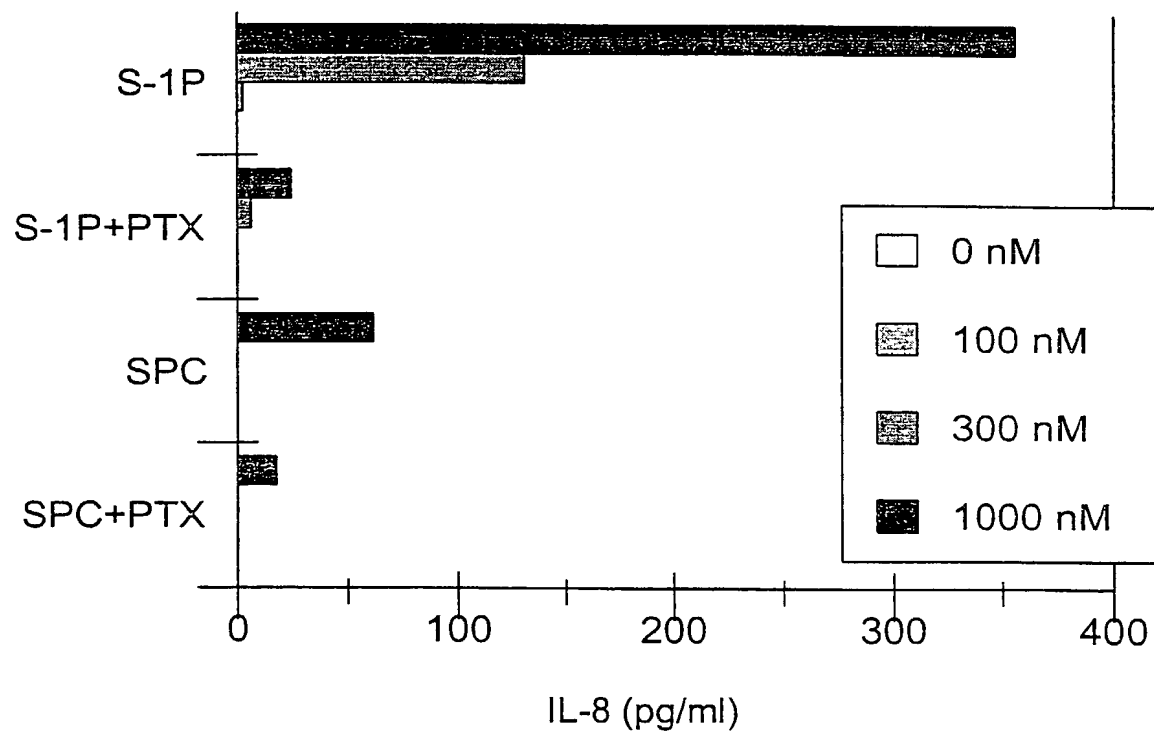


FIGURE 2 ~~8~~



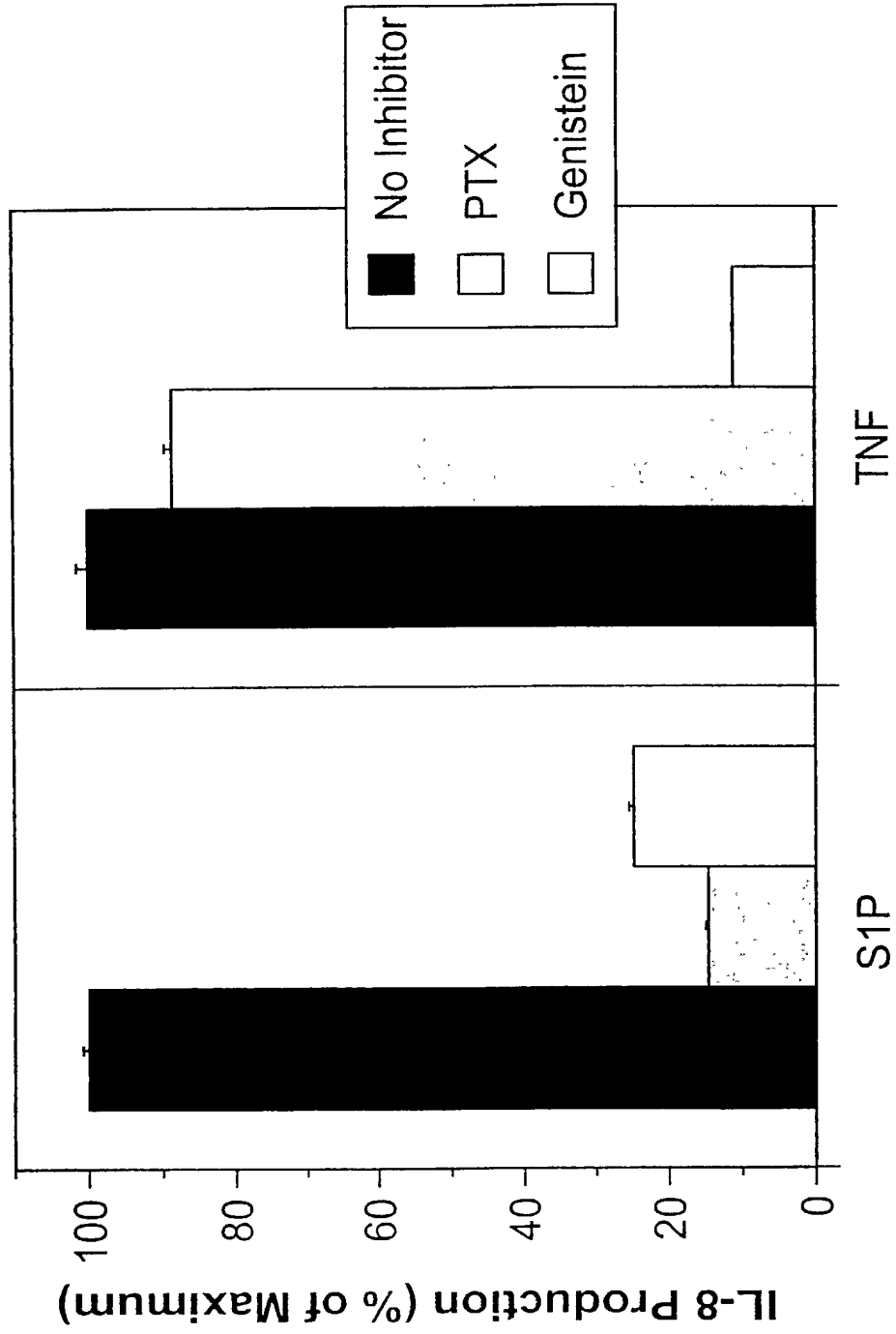


Figure 3.

FIGURE 4A

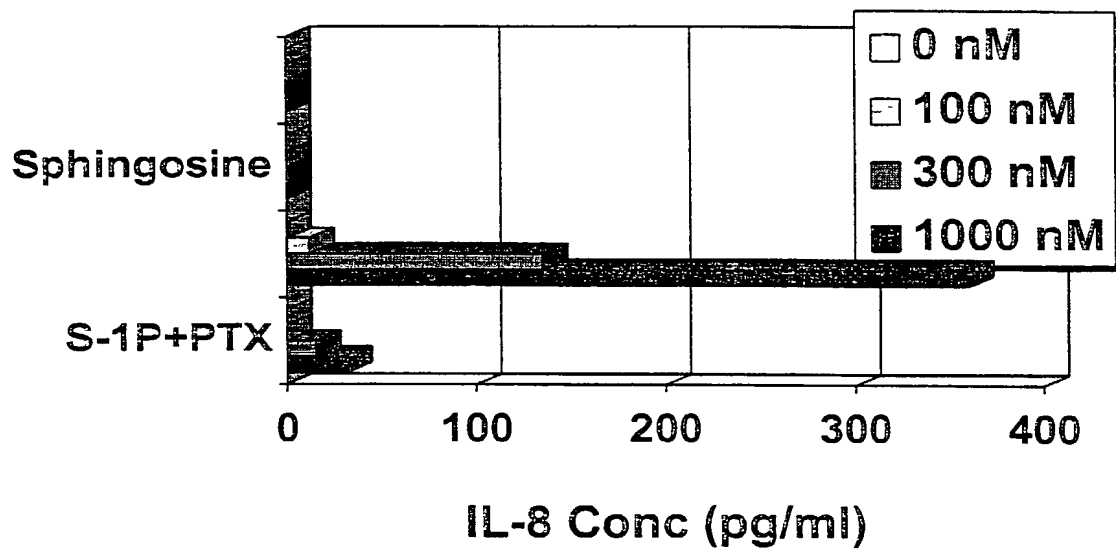


Figure 4B.

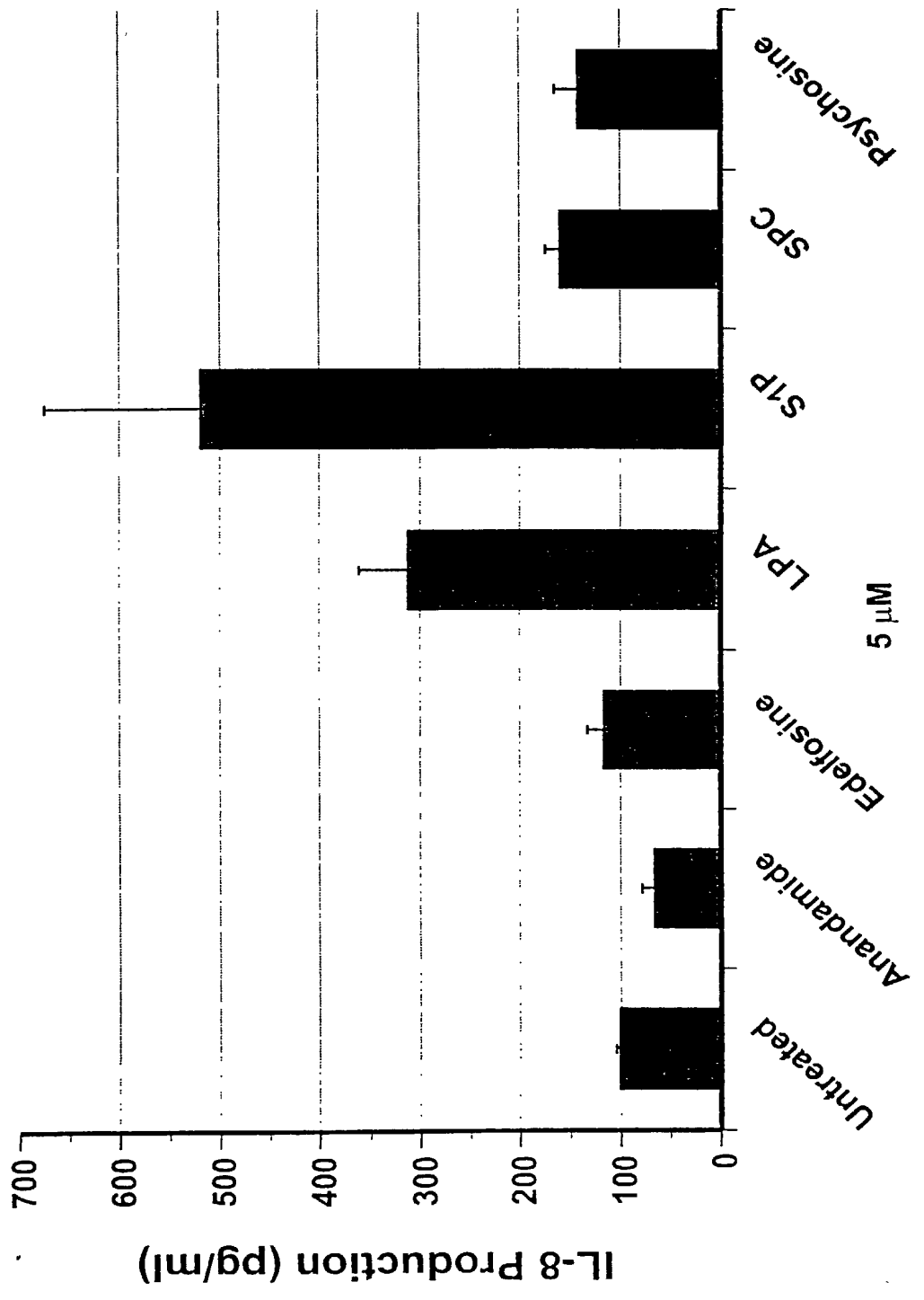


Figure 5.

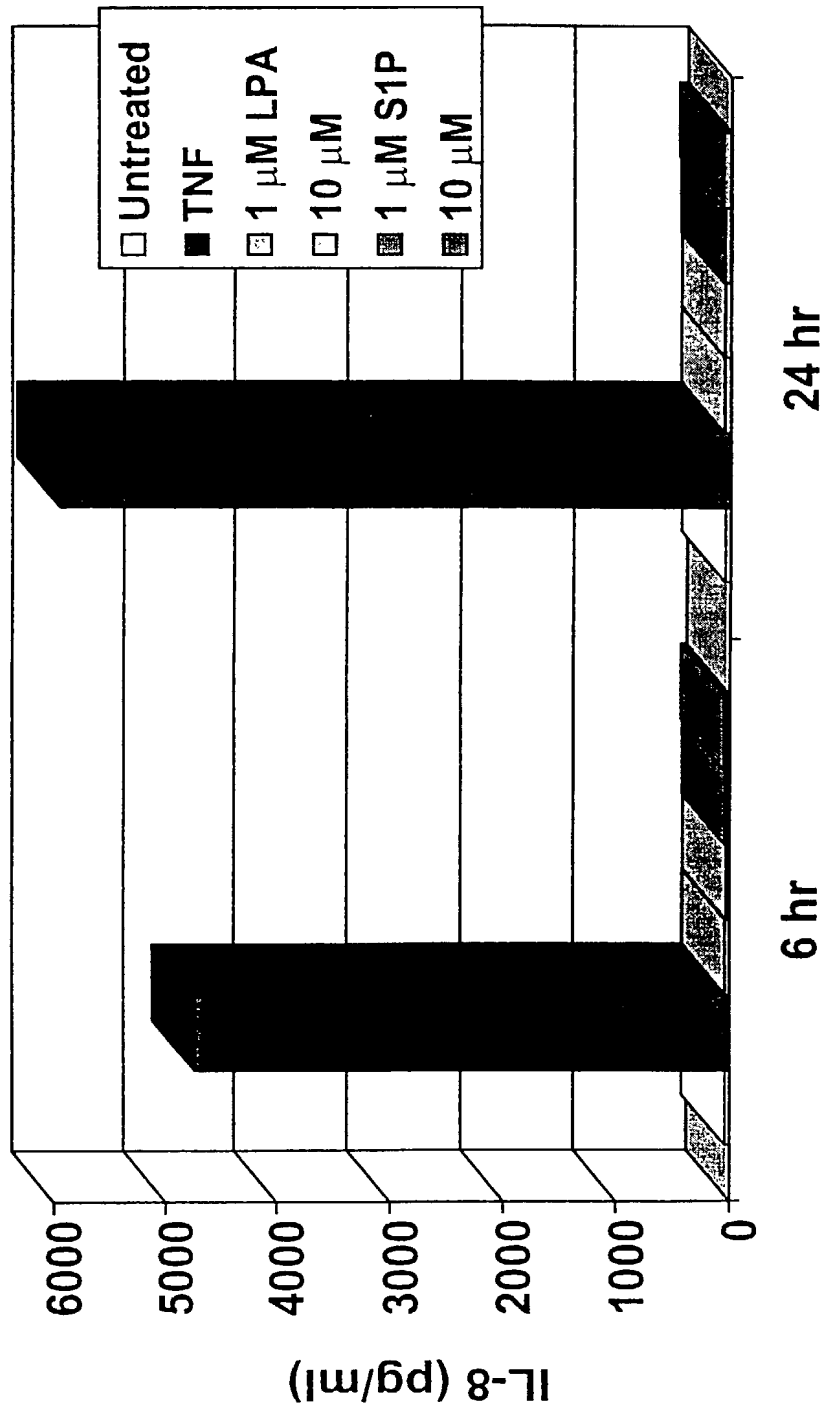
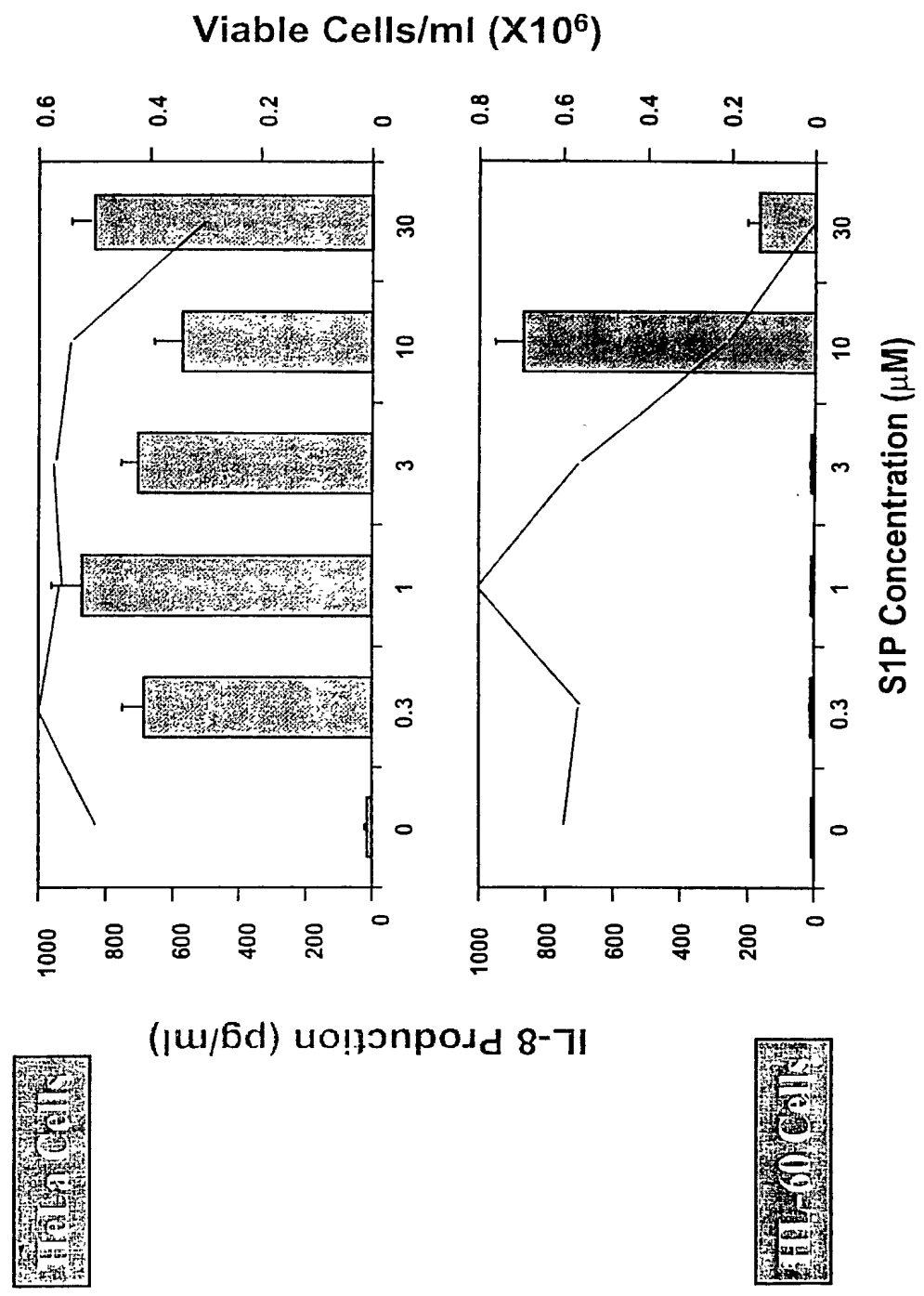




Figure 6.



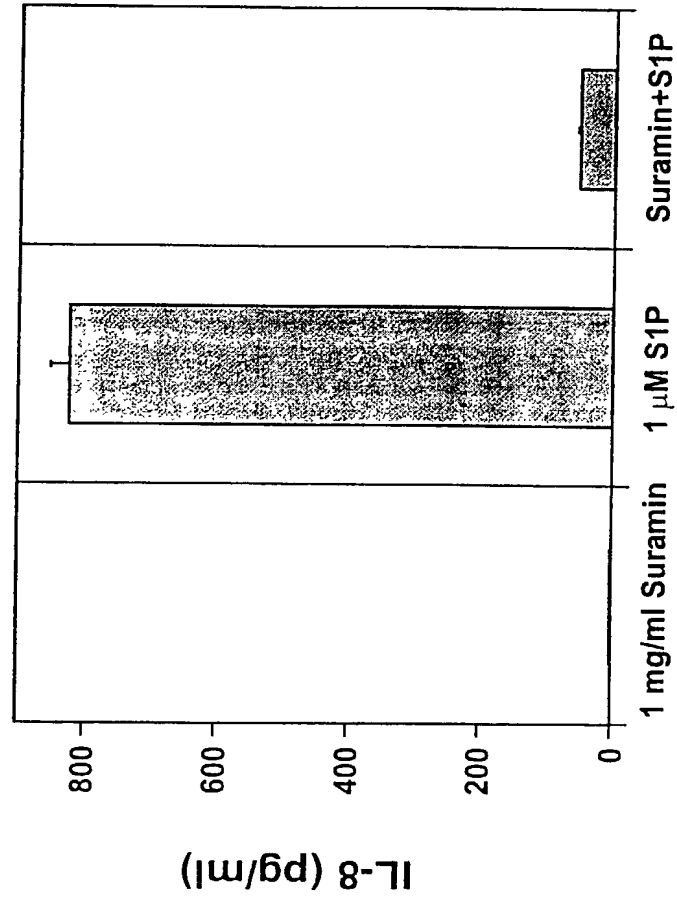


Figure 7.

Figure 8.

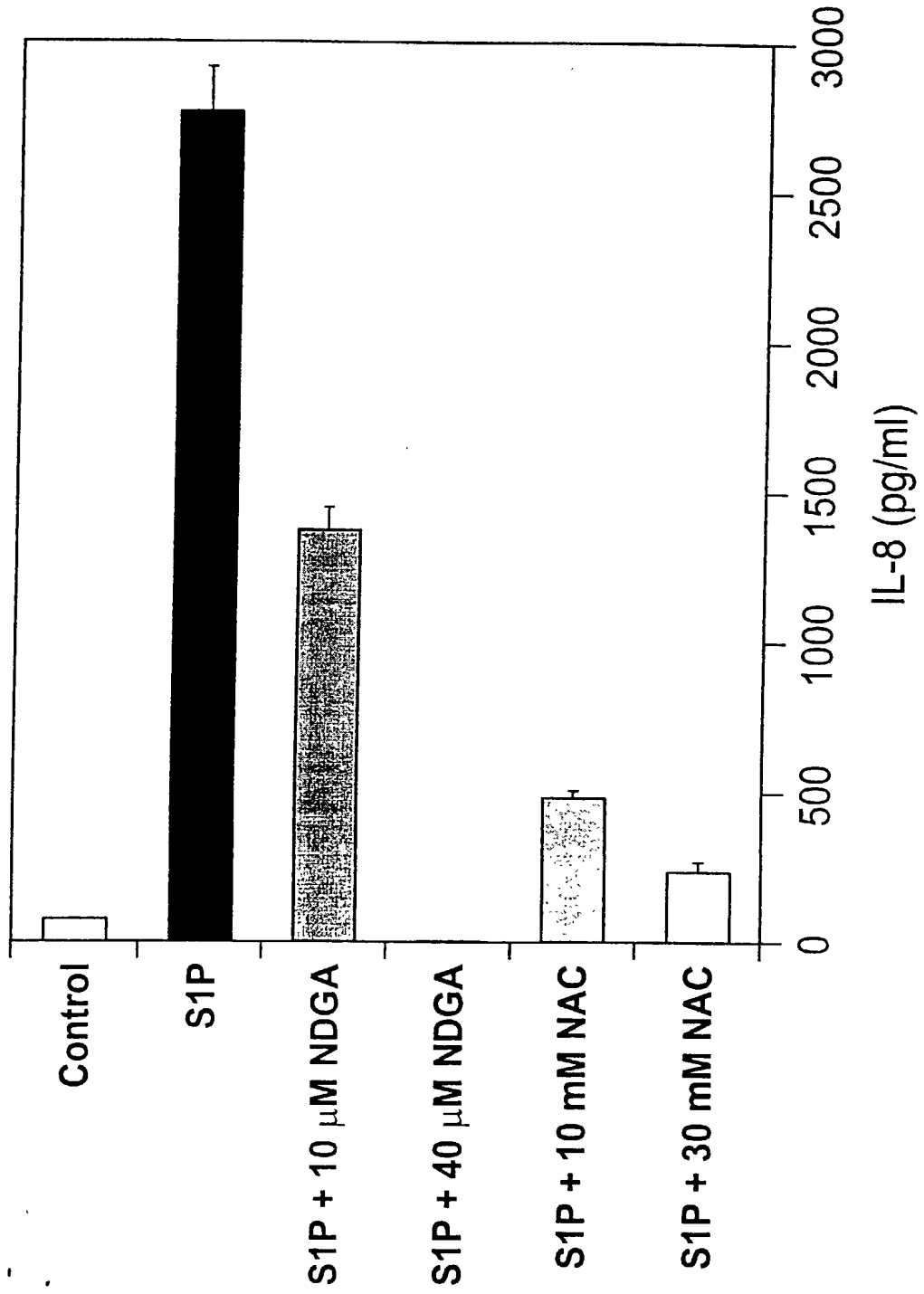


Figure 9.

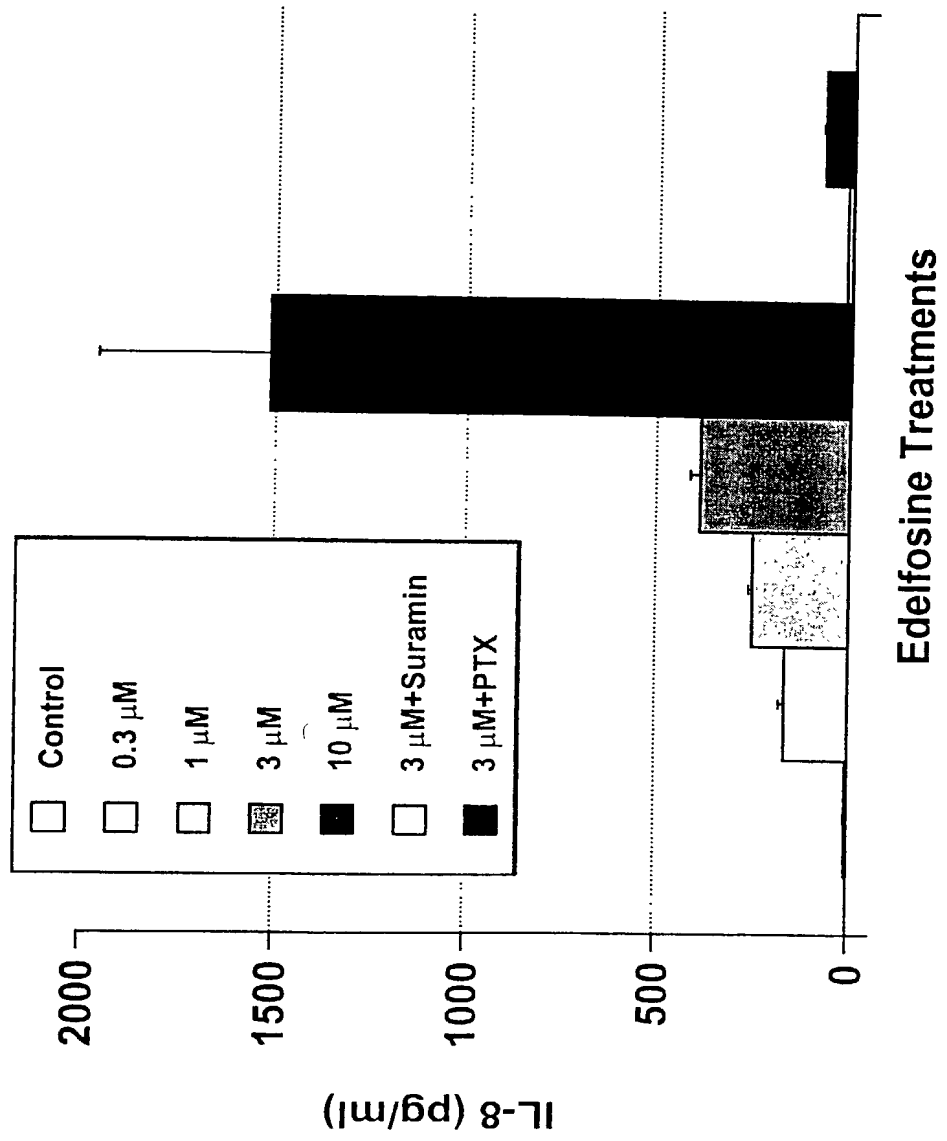


FIGURE 10A

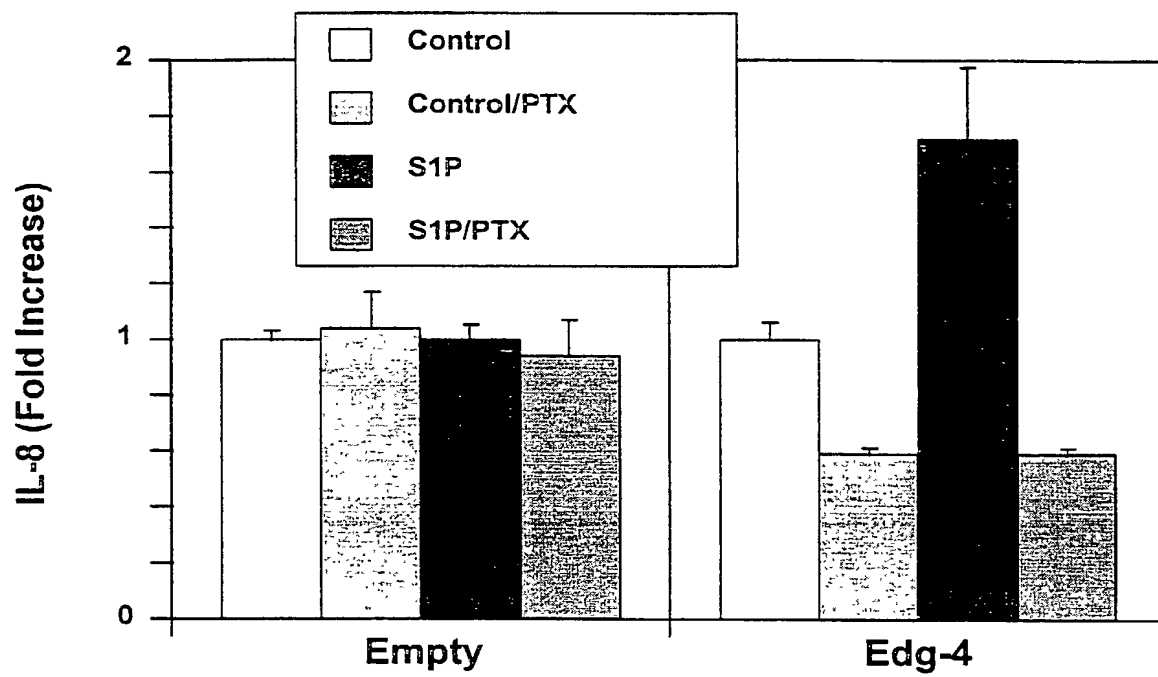


Figure 10B

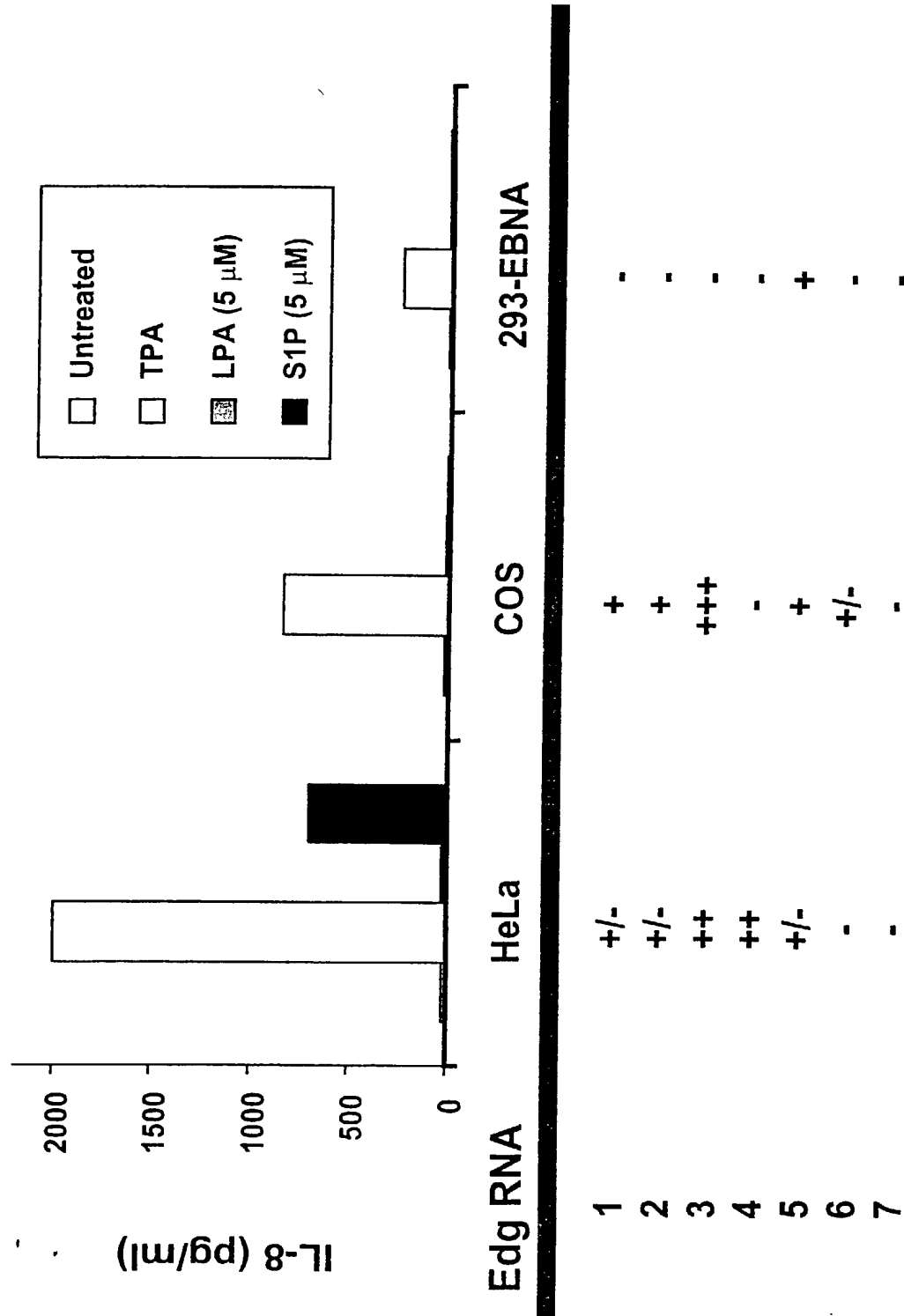


Figure 11.

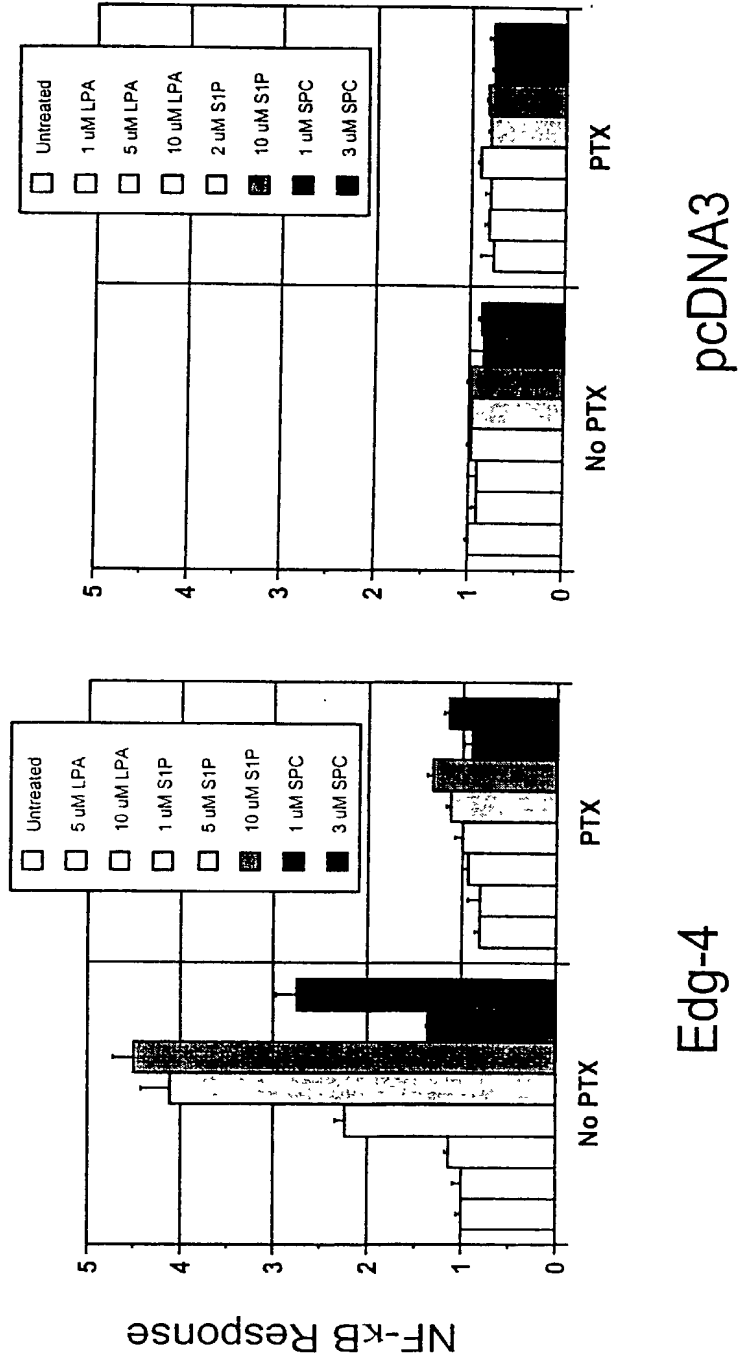


Figure 12.

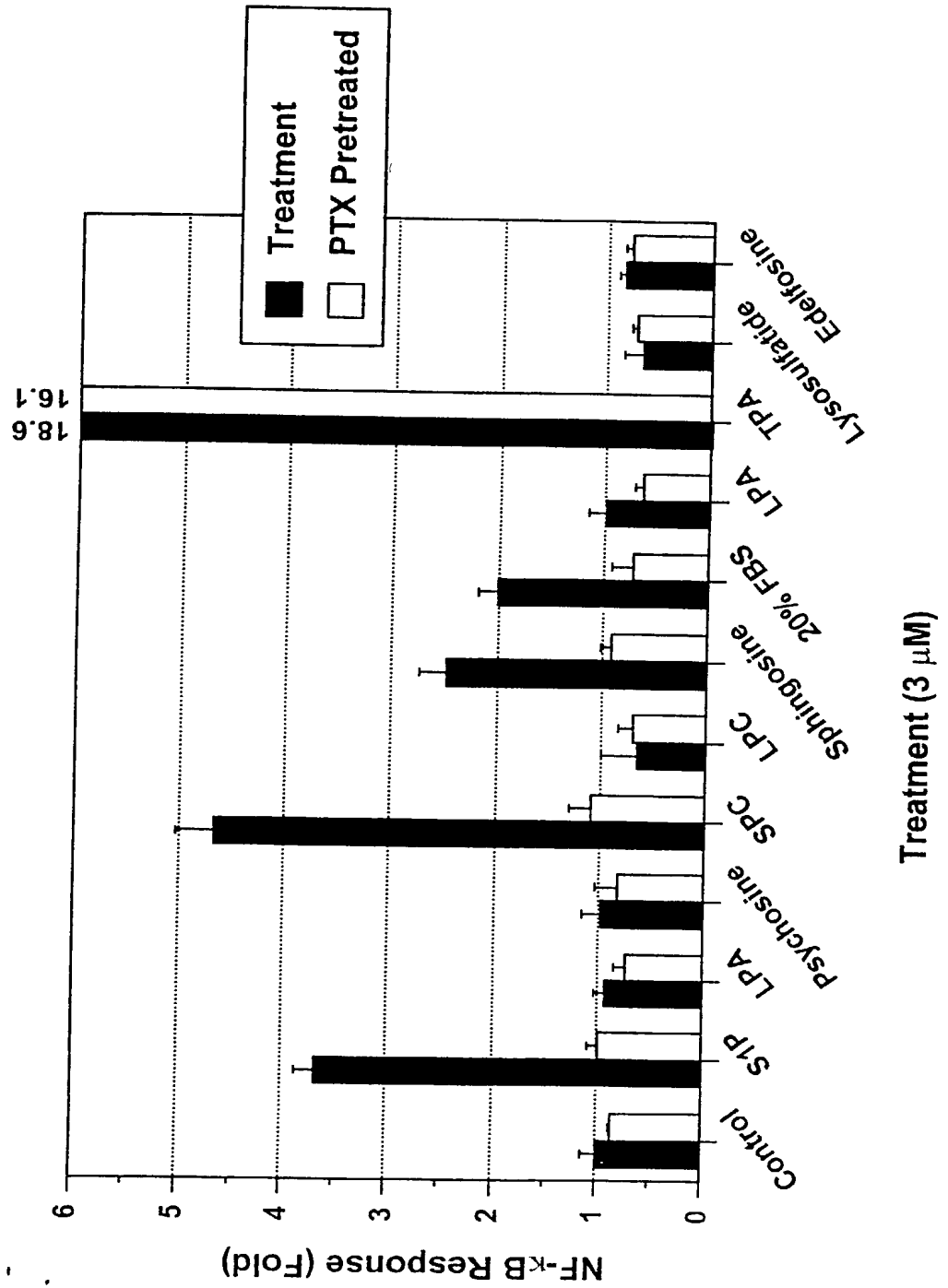




Figure 13.

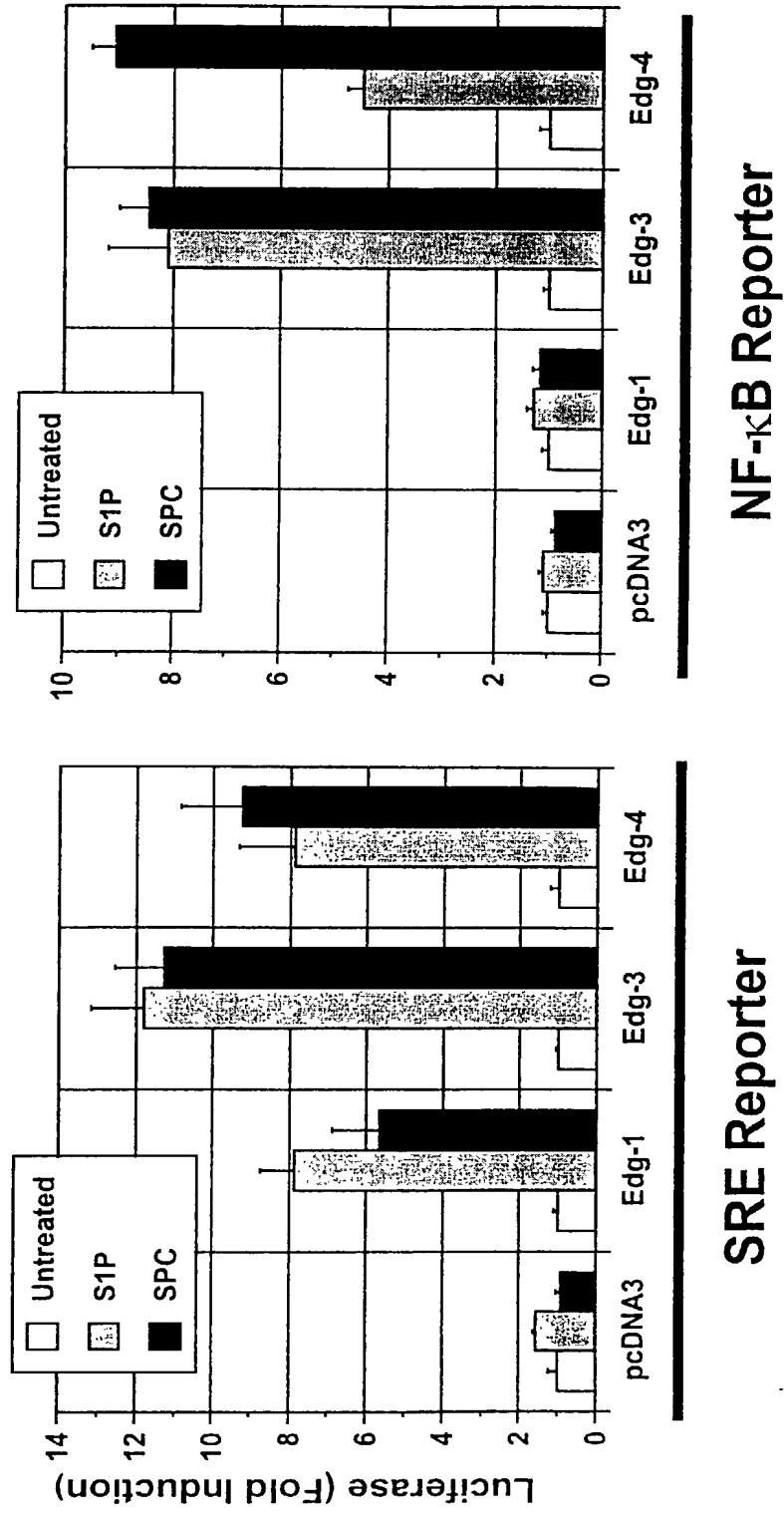


FIGURE 14

1				50	
AA834537	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC	CACCATGGGC
AA804628	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC	CACCATGGGC
AA827835	AGTTCTGAAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC	CACCATGGGC
	51				100
AA834537	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG	AACACTATAA
AA804628	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG	AACACTATAA
AA827835	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG	AACACTATAA
	101				150
AA834537	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC	CGCCAGGTGG
AA804628	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC	CGCCAGGTGG
AA827835	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC	CGCCAGGTGG
	151				200
AA834537	CCTCGGCATT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT	GGAAAACCTT
AA804628	CCTCGGCCTT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT	GGAAAACCTT
AA827835	GCTCGGCCTT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT	GGAAAACCTT
	201				250
AA834537	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT	CGGCAATGTA
AA804628	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT	CGGCAATGTA
AA827835	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT	CGGCAATGTA
	251				300
AA834537	CCTGTTTCTG	GGCAACCTGG	CCGCCTCCGA	TCTACTGGCA	GGCGTGGCCT
AA804628	CCTGTTTCTG	GGCAACCTGG	CCGCCTCCGA	TCTACTGGCA	GGCGTGGCCT
AA827835	CCTGTTTCTG	GGCAACCTGG	CCGCCTCCGA	TCTACTGGCA	GGCGTGG . CT
	301				350
AA834537	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG	GCTGACGCCT
AA804628	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG	GCTGACGCCT
AA827835	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG	GCTGACGCCT
	351				400
AA834537	GTGCAGTGGT	TTGCCC GGGA	CGGTCTGCCT	TCATCACGCT	CTCGGCCTCT
AA804628	GTGCAGTGGT	TTGCCC GGGA	C-----	-----	-----
AA827835	GTGCAGTGGT	TTGCCC GGGA	-----	-----	-----
	401				450
AA834537	GTCTTCAGCC	TCCTGGCCAT	CGCCATTGAG	CGCCACGTGG	CCATTGCAAA
AA804628	-----	-----	-----	-----	-----
AA827835	-----	-----	-----	-----	-----
	451				
AA834537	GG				
AA804628	--				
AA827835	--				

FIGURE 15 A

M G S L Y S E Y

```

1  AAAGCCCCATGGCCCCAGCAGGCCTCTGAGCCCCACCATGGGCAGCTTGTACTCGGAGTA
-----+-----+-----+-----+-----+-----+-----+-----+
60  TTTTCGGGGTACCGGGGTTCGTCCGGAGACTCGGGGTGGTACCCGTCGAACATGAGCCTCAT

    L N P N K V Q E H Y N Y T K E T L E T Q
61  CCTGAACCCCAACAAGGTCCAGGAACACTATAATTATACCAAGGAGACGCTGGAAACGCA
-----+-----+-----+-----+-----+-----+-----+
120  GGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATATGGTTCCTCTGCGACCTTTGCGT

    E T T S R Q V A S A F I V I L C C A I V
121  GGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATCGTCATCCTCTGTTGCGCCATTGT
-----+-----+-----+-----+-----+-----+-----+
180  CCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAGCAGTAGGAGACAACGCGGTAACA

    V E N L L V L I A V A R N S K F H S A M
181  GGTGGAACCTTCTGGTGCTCATTGCGGTGGCCCCGAAACAGCAAGTTCCTCTCGGCAAT
-----+-----+-----+-----+-----+-----+-----+
240  CCACCTTTTGGGAAGACCACGAGTAACGCCACCGGGCTTTGTCGTTCAAGGTGAGCCGTTA

    Y L F L G N L A A S D L L A G V A F V A
241  GTACCTGTTTCTGGGCAACCTGGCCGCTCCGATCTACTGGCAGGCGTGGCCTTCGTAGC
-----+-----+-----+-----+-----+-----+-----+
300  CATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGATGACCGTCCGCACCGGAAGCATCG

    N T L L S G S V T L R L T P V Q W F A R
301  CAATACCTTGCTCTCTGGCTCTGTACGCTGAGGCTGACGCCTGTGCAGTGGTTTGCCCCG
-----+-----+-----+-----+-----+-----+-----+
360  GTTATGGAACGAGAGACCGAGACAGTGCGACTCCGACTGCGGACACGTACCAAACGGGC

    E G S A F I T L S A S V F S L L A I A I
361  GGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTCTTCAGCCTCCTGGCCATCGCCAT
-----+-----+-----+-----+-----+-----+-----+
420  CCTCCCAGACGGAAGTAGTGCGAGAGCCGAGACAGAAGTCGGAGGACCGGTAGCGGTA

    E R H V A I A K V K L Y G S D K S C R M
421  TGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTATGGCAGCGACAAGAGCTGCCCGCAT
-----+-----+-----+-----+-----+-----+-----+
480  ACTCGCGGTGCACCGGTAACGGTTCCAGTTCGACATACCGTCGCTGTTCTCGACGGCGTA

    L L L I G A S W L I S L V L G G L P I L
481  GCTTCTGCTCATCGGGGCCTCGTGGCTCATCTCGCTGGTCCTCGGTGGCCTGCCCCATCCT
-----+-----+-----+-----+-----+-----+-----+
540  CGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGACCAGGAGCCACCGGACGGGTAGGA

    G W N C L G H L E A C S T V L P L Y A K
541  TGGCTGGAACCTGCCTGGGCCACCTCGAGGCTGCTCCACTGTCTGCCTCTCTACGCCAA
-----+-----+-----+-----+-----+-----+-----+
600  ACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGGTGACAGGACGAGAGATGCGGTT

    H Y V L C V V T I F S I I L L A I V A L
601  GCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATCATCCTGTTGGCCATCGTGGCCCT
-----+-----+-----+-----+-----+-----+-----+
660  CGTAATACAGACACGCACCACTGGTAGAAGAGGTAGTAGGACAACCGGTAGCACCGGGA

```

Y V R I Y C V V R S S H A D M A A P Q T  
 661 GTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCACGCTGACATGGCCGCCCCGAGAC 720  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CATGCACGCGTAGATGACGCACCAGGCGAGTTCGGTGCGACTGTACCGGCGGGGCGTCTG  
  
 L A L L K T V T I V L G V F I V C W L P  
 721 GCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGCGTCTTTATCGTCTGCTGGCTGCC 780  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCGCAGAAATAGCAGACGACCGACGG  
  
 A F S I L L L D Y A C P V H S C P I L Y  
 781 CGCCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCCGTCCACTCCTGCCGATCCTCTA 840  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGGCAGGTGAGGACGGGCTAGGAGAT  
  
 K A H Y X F A V S T L N S L L N P V I Y  
 841 CAAAGCCCACTACYTTCGCGCTCTCCACCCTGAATTCCCTGCTCAACCCCGTCATCTA 900  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GTTTCGGGTGATGRAAAAGCGGCAGAGGTGGGACTTAAGGGACGAGTTGGGGCAGTAGAT  
  
 T W R S R D L R R E V L R P L Q C W R P  
 901 CACGTGGCGCAGCCGGGACCTGCGGCGGGAGGTGCTTCGGCCGCTGCAGTGCTGGCGGCC 960  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GTGCACCGCGCTCGGCCCTGGACGCCGCCCTCCACGAAGCCGGCGACGTNACGACCGCCGG  
  
 G V G V Q G R R R G G T P G H H L L P L  
 961 GGGGGTGGGGGTGCAAGGACGGAGGCGGGGCGGGACCCCGGGCCACCACCTCCTGCCACT 1020  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CCCCCACCCCCACGTTCTGCCTCCGCCCCGCCCTGGGGCCCCGGTGGTGGAGGACGGTGA  
  
 R S S S S L E R G M H M P T S P T F L E  
 1021 CCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATGCCACGTCACCCACGTTTCTGGA 1080  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GGCGTCGAGGTCGAGGGACCTCTCCCCGTACGTGTACGGGTGCAGTGGGTGAAAAGACCT  
  
 G N T V V \*  
 1081 GGGCAACACGGTGGTCTGAGGGTGGGGTGGACCAACAACCAGGCCAGGGCATAGGGGTT 1140  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CCCGTTGTGCCACCAGACTCCCACCCCCACCTGGTTGTTGGTCCGGTCCCGTATCCCCAA  
  
 CATGGAAAGGCCACTGGGTGACCCCAAATA  
 1141 -----+-----+-----+-----+ 1170  
 GTACCTTTCCGGTGACCCACTGGGGTTTAT

**Figure 15B**

**cDNA sequence of clone pC3-hedg4#36 encoding functional HEDG4 receptor protein.**

```

1  ATGGGCAGCTTGTACTCGGAGTACCTGAACCCCAACAAGGTCCAGGAACACTATAATTAT  60
   -----+-----+-----+-----+-----+-----+-----+
   TACCCGTCGAACATGAGCCTCATGGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATA

61  ACCAAGGAGACGCTGGAAACGCAGGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATC  120
   -----+-----+-----+-----+-----+-----+-----+
   TGGTTCCTCTGCGACCTTTGCGTCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAG

121  GTCATCCTCTGTTGCGCCATTGTGGTGGAAAACCTTCTGGTGCTCATTGCGGTGGCCCCGA  180
   -----+-----+-----+-----+-----+-----+-----+
   CAGTAGGAGACAACGCGGTAACACCACCTTTTGGGAAGACCACGAGTAACGCCACCGGGCT

181  AACAGCAAGTTCCACTCGGCAATGTACCTGTTTTCTGGGCAACCTGGCCGCCTCCGATCTA  240
   -----+-----+-----+-----+-----+-----+-----+
   TTGTCGTTCAAGGTGAGCCGTTACATGGACAAAGACCCGTTGACCGGCGGAGGCTAGAT

241  CTGGCAGGCGTGGCCTTCGTAGCCAATACCTTGCTCTCTGGCTCTGTCACGCTGAGGCTG  300
   -----+-----+-----+-----+-----+-----+-----+
   GACCGTCCGCACCGGAAGCATCGGTTATGGAACGAGAGACCGAGACAGTGCGACTCCGAC

301  ACGCCTGTGCAGTGGTTTGCCCGGGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTC  360
   -----+-----+-----+-----+-----+-----+-----+
   TGCGGACACGTCACCAAACGGGCCCTCCCGAGACGGAAGTAGTGCGAGAGCCGGAGACAG

361  TTCAGCCTCCTGGCCATCGCCATTGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTAT  420
   -----+-----+-----+-----+-----+-----+-----+
   AAGTCGGAGGACCGGTAGCGGTAACCTCGCGGTGCACCGGTAACGGTTCAGTTCGACATA

421  GGCAGCGACAAGAGCTGCCGCATGCTTCTGCTCATCGGGGCCTCGTGGCTCATCTCGCTG  480
   -----+-----+-----+-----+-----+-----+-----+
   CCGTTCGCTGTTCTCGACGGCGTACGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGAC

481  GTCCTCGGTGGCCTGCCCATCCTTGGCTGGAAGTGCCTGGGCCCACCTCGAGGCCTGCTCC  540
   -----+-----+-----+-----+-----+-----+-----+
   CAGGAGCCACCGGACGGGTAGGAACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGG

541  ACTGTCCTGCCTCTCTACGCCAAGCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATC  600
   -----+-----+-----+-----+-----+-----+-----+
   TGACAGGACGGAGAGATGCGGTTTCGTAATACACGACACGCACCACTGGTAGAAGAGGTAG

601  ATCCTGTTGGCCGTCGTGGCCCTGTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCAC  660
   -----+-----+-----+-----+-----+-----+-----+
   TAGGACAACCGGCAGCACCGGGACATGCACGCGTAGATGACGCACCAGGCGAGTTCGGTG

661  GCTGACATGGCCGCCCCGACAGCGCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGC  720
   -----+-----+-----+-----+-----+-----+-----+
   CGACTGTACC GGCGGGGCGTCTGCGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCG

721  GTCTTTATCGTCTGCTGGCTGCCCCGCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCC  780
   -----+-----+-----+-----+-----+-----+-----+

```



## FIGURE 16 A

1 MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE  
 51 NLLVLIIVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLGGSVTLRLL  
 101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL  
 151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI  
 201 ILLAIVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF  
 251 SILLLDYACP VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL  
 301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN  
 351 TVV\*

Conserved features of G-protein coupled receptors include:

N-terminal extracellular domain:	Residues 1 - 36
TM-I:	Residues 37 - 57
Intracellular loop 1:	Residues 58 - 68
TM-II:	Residues 69 - 92
Extracellular loop 1:	Residues 93 - 111
TM-III:	Residues 112 - 130
Intracellular loop 2:	Residues 131 - 149
TM-IV:	Residues 150 - 168
Extracellular loop 2:	Residues 169 - 185
TM-V:	Residues 186 - 210
Intracellular loop 3:	Residues 211 - 232
TM-VI:	Residues 233 - 254
Extracellular loop 3:	Residues 255 - 266
TM-VII:	Residues 267 - 285
C-terminal cytoplasmic domain:	Residues 286 - 353

Potential post-transcriptional modification sites:

N-glycosylation:	Residues 19
Phosphorylation:	Residues 142, 145, 219, 289, 332, 345
Myristylation:	Residues 141, 318

**Figure 16B**

**Predicted amino acid sequence of HEDG4 polypeptide encoded by pC3-hedg4#36.**

```
1  MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
51  NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
201 ILLAVVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF
251 SILLLDYACP VHSCPILYKA HYLFAVSTLN SLLNPVIYTW RSRDLRREVL
301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN
351 TVV
```



FIGURE 17 A

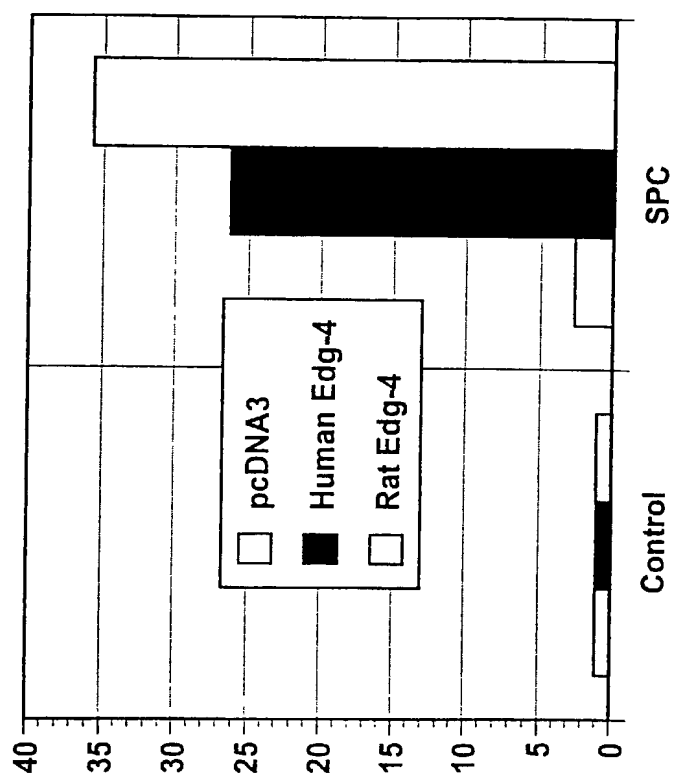
Human	1	MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVE	50
		:          :	
Rat	1	MGGLYSEYLNPEKVQEHYNYTKETLDMQETPSRKVASAFIIILCCAIVVE	50
Human	51	NLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRL	100
Rat	51	NLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSL	100
Human	101	TPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVLYGSDKSCRMLL	150
		.   :	
Rat	101	TPLQWFAREGSAFITLSASVFSLLAIAIERQVAIAKVLYGSDKSCRMLM	150
Human	151	LIGASWLISLVLGGPLILGWNCLGHLEACSTVLPYAKHYVLCVVTIFSI	200
		:   :	
Rat	151	LIGASWLISLILGGPLILGWNCLDHLEACSTVLPYAKHYVLCVVTIFSV	200
Human	201	ILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLGVFIVCWLPAP	250
		:	
Rat	201	ILLAIVALYVRIYFVVRSSHADVAGPQTLALLKTVTIVLGVFIICWLPAF	250
Human	251	SILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL	300
		:	
Rat	251	SILLLDSTCPVRACPVLYKAHYFFAFATLNSLLNPVIYTWRSRDLRREVL	300
Human	301	RPLQCWRPGVGVGQRRRGTPGHLLPLRSSSSSLERGMHMPSTPTFLEGN	350
Rat	301	RPLLCWRQKGKATG.RRGGNPGHRLPLRSSSSSLERGLHMPSTPTFLEGN	349
Human	351	TVV* 353	
Rat	350	TVV* 352	

Figure 17B

**Alignment of HEDG4 with pC3-hedg4#36 translation product and rat H218 (REDG4).** Differences between pC3-hedg4#36 translation product and previously determined HEDG4 polypeptide are indicated in reverse text. Differences between rat and human edg-4 polypeptide sequences are shown in bold, shaded text.

	1				50
HEDG4	MGSLYSEYLN	PNKVQEHYNY	TKETLETQET	TSRQVASAFI	VILCCAIVVE
HEDG4#36	MGSLYSEYLN	PNKVQEHYNY	TKETLETQET	TSRQVASAFI	VILCCAIVVE
REDG4	MGGLYSEYLN	PEKVQEHYNY	TKETLDMQET	PSRKVASAFI	ILCCAIVVE
	51				100
HEDG4	NLLVLIAVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT	LLSGSVTLRL
HEDG4#36	NLLVLIAVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT	LLSGSVTLRL
REDG4	NLLVLIAVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT	LLSGPVTLSL
	101				150
HEDG4	TPVQWFAREG	SAFITLSASV	FSLLAIAIER	HVAIAKVKLY	GSDKSCRMLL
HEDG4#36	TPVQWFAREG	SAFITLSASV	FSLLAIAIER	HVAIAKVKLY	GSDKSCRMLL
REDG4	TPVQWFAREG	SAFITLSASV	FSLLAIAIER	QVAIAKVKLY	GSDKSCRMLM
	151				200
HEDG4	LIGASWLISL	VLGGLPILGW	NCLGHLEACS	TVLPLYAKHY	VLCVVTIFSI
HEDG4#36	LIGASWLISL	VLGGLPILGW	NCLGHLEACS	TVLPLYAKHY	VLCVVTIFSI
REDG4	LIGASWLISL	ELGGLPILGW	NCLDHLEACS	TVLPLYAKHY	VLCVVTIFSV
	201				250
HEDG4	ILLAVVALYV	RIYCVVRSSH	ADMAAPQTLA	LLKTVTIVLG	VFIVCWLPAP
HEDG4#36	ILLAVVALYV	RIYCVVRSSH	ADMAAPQTLA	LLKTVTIVLG	VFIVCWLPAP
REDG4	ILLAIIVALYV	RIYFVVRSSH	ADVAGPQTLA	LLKTVTIVLG	VFIIICWLPAP
	251				300
HEDG4	SILLLDYACP	VHSCPILYKA	HYXFAVSTLN	SLLNPVIYTW	RSRDLRREVL
HEDG4#36	SILLLDYACP	VHSCPILYKA	HYXFAVSTLN	SLLNPVIYTW	RSRDLRREVL
REDG4	SILLLDSTCP	VRACPVLKYA	HYFFAFATLN	SLLNPVIYTW	RSRDLRREVL
	301				350
HEDG4	RPLQCWRPGV	GVQGRRRGGT	PGHLLPLRS	SSSLERGMHM	PTSPTFLEGN
HEDG4#36	RPLQCWRPGV	GVQGRRRGGT	PGHLLPLRS	SSSLERGMHM	PTSPTFLEGN
REDG4	RPLLCWRQK	GATG.RRGGN	PGHRLPLRS	SSSLERGLHM	PTSPTFLEGN
	351				
HEDG4	TVV-				
HEDG4#36	TVV-				
REDG4	TVV-				

Figure 18A.



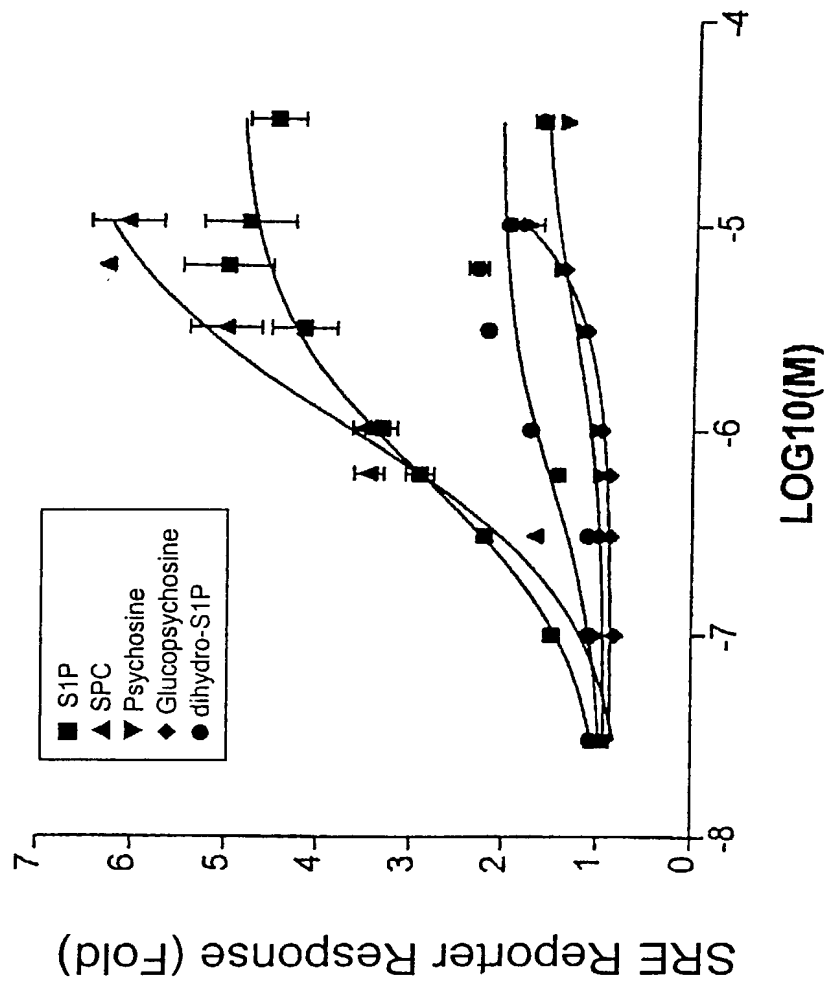
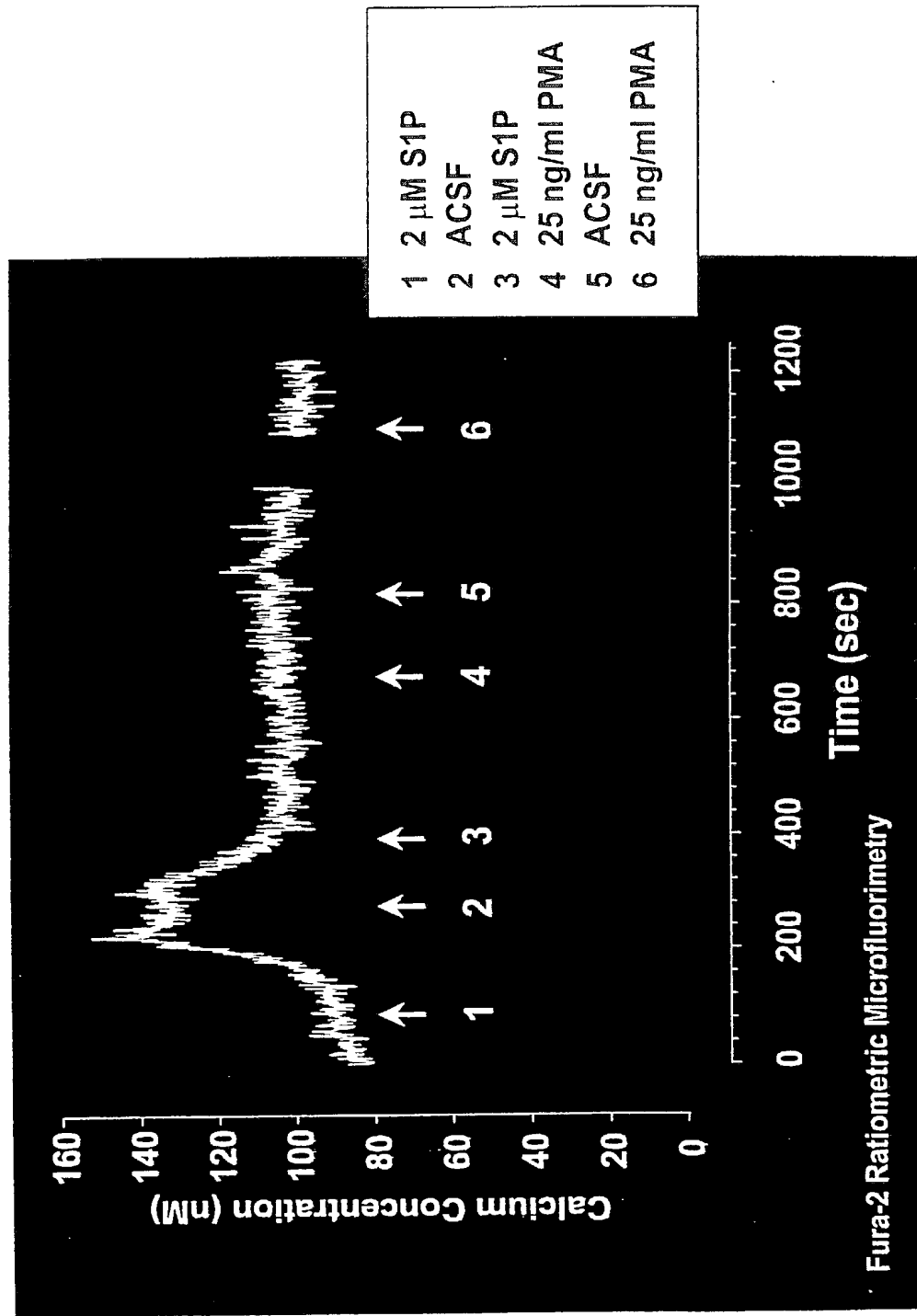


Figure 18B.

Figure 19.



10094507.051402

Figure 20.

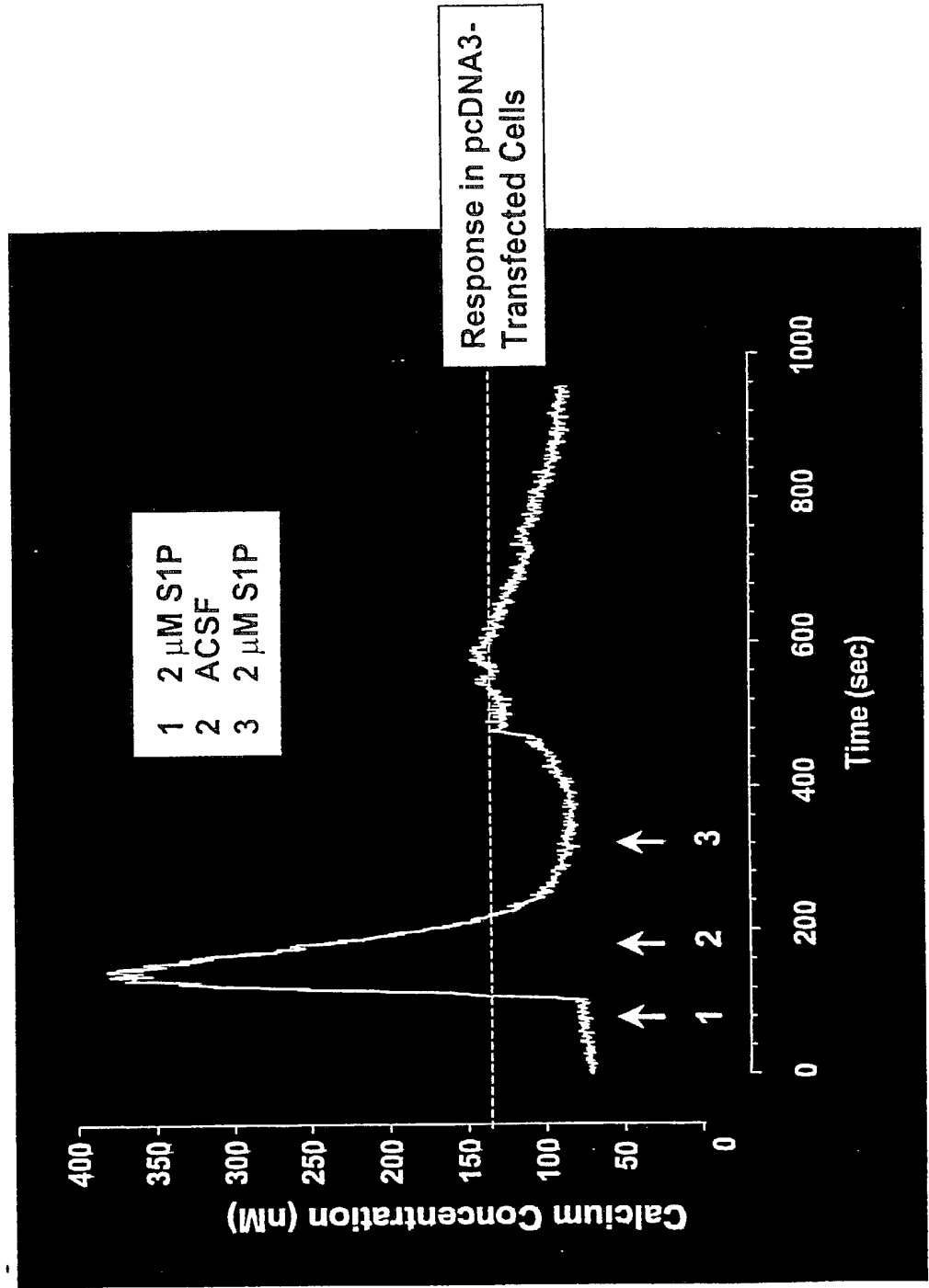


Figure 21. Human Edg-6 Amino Acid Sequence.

```

      MVIMGQCYNETIGFFYNNSGKELSSHWRPKDVVVVALGLTVSVLVLLTNLLVIAAIASN
1  -----+-----+-----+-----+-----+-----+-----+
                                     60
      RRFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVA
61 -----+-----+-----+-----+-----+-----+-----+
                                     120
      TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVVVAALGLGLLPAHSWHCLCALDRCSR
121 -----+-----+-----+-----+-----+-----+-----+
                                     180
      MAPLLSRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQMAEHVSCHPRYRETTLSLV
181 -----+-----+-----+-----+-----+-----+-----+
                                     240
      KTVVIIILGAFVVCWTPGQVVLDDGLGCESC�VLAVEKYFLLAEANSLVNAAVYSCRDA
241 -----+-----+-----+-----+-----+-----+-----+
                                     300
      EMRRTFRRLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMDSTL*
301 -----+-----+-----+-----+-----+-----+-----+
                                     352

```

Figure 22. Human Edg-6 Sequence

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1  ATGGTCATCATGGGCCAGTGCTACTACAACGAGACCATCGGCTTCTTCTATAACAACAGT
   -----+-----+-----+-----+-----+-----+-----+
61 TACCAGTAGTACCCGGTCACGATGATGTTGCTCTGGTAGCCGAAGAAGATATTGTTGTCA
   -----+-----+-----+-----+-----+-----+-----+
   GGCAAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGGTCGTGGTGGCACTGGGGCTG
61 -----+-----+-----+-----+-----+-----+-----+
   CCGTTTCTCGAGTCGAGGGTGACCGCCGGGTTCTTACACCAGCACCACCGTGACCCGAC
   -----+-----+-----+-----+-----+-----+-----+
121 ACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCATAGCAGCCATCGCCTCCAAC
   -----+-----+-----+-----+-----+-----+-----+
   TGGCAGTCGCACGACCACGACGACTGGTTAGACGACCAGTATCGTCGGTAGCGGAGGTTG
   -----+-----+-----+-----+-----+-----+-----+
181 CGCCGCTTCCACCAGCCCATCTACTACCTGCTCGGCAATCTGGCCGCGGCTGACCTCTTC
   -----+-----+-----+-----+-----+-----+-----+
   GCGGCGAAGGTGGTCGGGTAGATGATGGACGAGCCGTTAGACCGGCGCCGACTGGAGAAG
   -----+-----+-----+-----+-----+-----+-----+
241 GCGGGCGTGCCCTACCTCTTCCTCATGTTCCACACTGGTCCCCGCACAGCCCGACTTTCA
   -----+-----+-----+-----+-----+-----+-----+
   CGCCCGCACCGGATGGAGAAGGAGTACAAGGTGTGACCAGGGGCGTGTGCGGCTGAAAGT
   -----+-----+-----+-----+-----+-----+-----+
301 CTTGAGGGCTGGTTCTTCTGCGGCAGGGCTTGCTGGACACAAGCCTCACTGCGTCGGTGGCC
   -----+-----+-----+-----+-----+-----+-----+
   GAACTCCCCGACCAAGGACGCCGTCCCGAACGACCTGTGTTCTGGAGTGACGCAGCCACCGG
   -----+-----+-----+-----+-----+-----+-----+
361 ACACTGCTGGCCATCGCCGTGGAGCGGCACCGCAGTGTGATGGCCGTGCAGCTGCACAGC
   -----+-----+-----+-----+-----+-----+-----+
   TGTGACGACCGGTAGCGGCACCTCGCCGTGGCGTCACACTACCGGCACGTGCAGCTGTGCG
   -----+-----+-----+-----+-----+-----+-----+
421 CGCCTGCCCCGTGGCCGCGTGGTCATGCTCATTGTGGGCGTGTGGGTGGCTGCCCTGGGC
   -----+-----+-----+-----+-----+-----+-----+
   GCGGACGGGGCACCGGCGCACCAGTACGAGTAACACCCGCACACCCACCGACGGGACCCG
   -----+-----+-----+-----+-----+-----+-----+
481 CTGGGGCTGCTGCCTGCCCCTCTGGCACTGCCTCTGTGCCCTGGACCGCTGCTCACGC
   -----+-----+-----+-----+-----+-----+-----+
   GACCCCGACGACGGACGGGTGAGGACCGTGACGGAGACACGGGACCTGGCGACGAGTGCG
   -----+-----+-----+-----+-----+-----+-----+
541 ATGGCACCCCTGCTCAGCCGCTCCTATTTGGCCGTCTGGGCTCTGTGAGCCTGCTTGTC
   -----+-----+-----+-----+-----+-----+-----+
   TACCGTGGGGACGAGTCGGCGAGGATAAACCGGCAGACCCGAGACAGCTCGGACGAACAG
   -----+-----+-----+-----+-----+-----+-----+
601 TTCCTGCTCATGGTGGCTGTGTACACCCGATTTTCTTCTACGTGCGGCGGCGAGTGCAG
   -----+-----+-----+-----+-----+-----+-----+
   AAGGACGAGTACCACCGACACATGTGGGCGTAAAAGAAGATGCACGCCGCCGCTCACGTC
   -----+-----+-----+-----+-----+-----+-----+
661 CGCATGGCAGAGCATGTGAGCTGCCACCCCGCTACCGAGAGACCACGCTCAGCCTGGTC
   -----+-----+-----+-----+-----+-----+-----+
   GCGTACCGTCTCGTACAGTCGACGGTGGGGGCGATGGCTCTCTGGTGCGAGTCGGACCAG
   -----+-----+-----+-----+-----+-----+-----+
721 AAGACTGTTGTTCATCATCCTGGGGGCGTTCGTGGTCTGCTGGACACCAGGCCAGGTGGTA
   -----+-----+-----+-----+-----+-----+-----+
   TTCTGACAACAGTAGTAGGACCCCCGCAAGCACCAGACGACCTGTGGTCCGGTCCACCAT
   -----+-----+-----+-----+-----+-----+-----+
781 CTGCTCCTGGATGGTTTAGGCTGTGAGTCCTGCAATGTCTGGCTGTAGAAAAGTACTTC
   -----+-----+-----+-----+-----+-----+-----+
   GACGAGGACCTACCAAATCCGACACTCAGGACGTTACAGGACCGACATCTTTTCATGAAG
   -----+-----+-----+-----+-----+-----+-----+

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      C T A C T G c T G G C C G A G G C C A A C T C A C T G G T C A A T G C T G C T G T G T A C T C T T G C C G A G A T G C T
841  -----+-----+-----+-----+-----+-----+
      G A T G A C g A C C G G C T C C G G T T G A G T G A C C A G T T A C G A C G A C A C A T G A G A A C G G C T C T A C G A
                                     900

      G A G A T G C G C C G C A C C T T C C G C C G C C T T C T C T G C T G C G C G T G C C T C C G C C A G T C C A C C C G C
901  -----+-----+-----+-----+-----+-----+
      C T C T A C G C G G C G T G G A A G G C G G C G G A A G A G A C G A C G C G C A C G G A G G C G G T C A G G T G G G C G
                                     960

      G A G T C T G T C C A C T A T A C A T C C T C T G C C C A G G G A G G T G C C A G C A C T C G C A T C A T G C T T C C C
961  -----+-----+-----+-----+-----+-----+
      C T C A G A C A G G T G A T A T G T A G G A G A C G G G T C C C T C C A C G G T C G T G A G C G T A G T A C G A A G G G
                                     1020

      G A G A A C G G C C A C C C A C T G A T G G A C T C C A C C C T T T A G
1021 -----+-----+-----+-----+-----+
      C T C T T G C C G G T G G G T G A C T A C C T G A G G T G G G A A A T C
                                     1056

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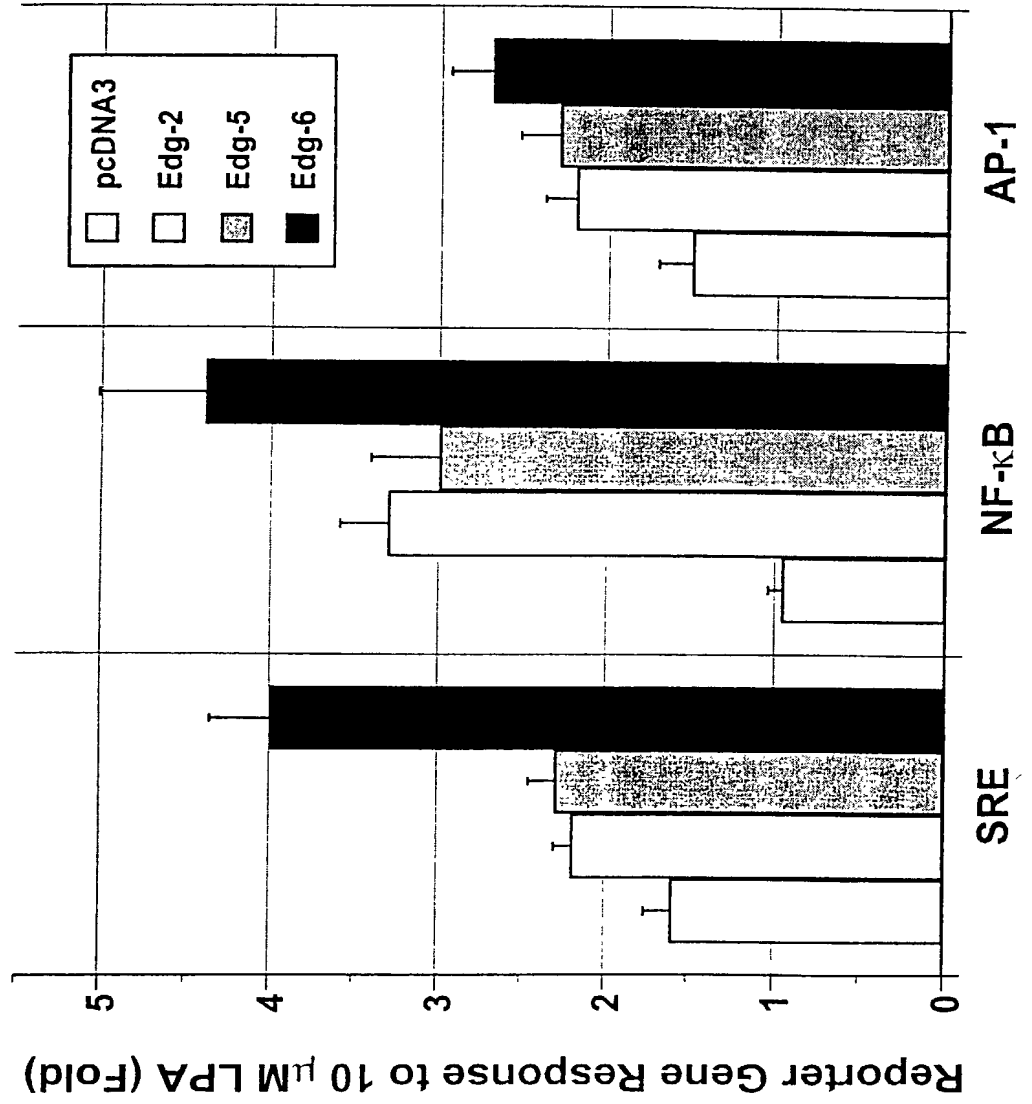


Figure 23.

Figure 24.

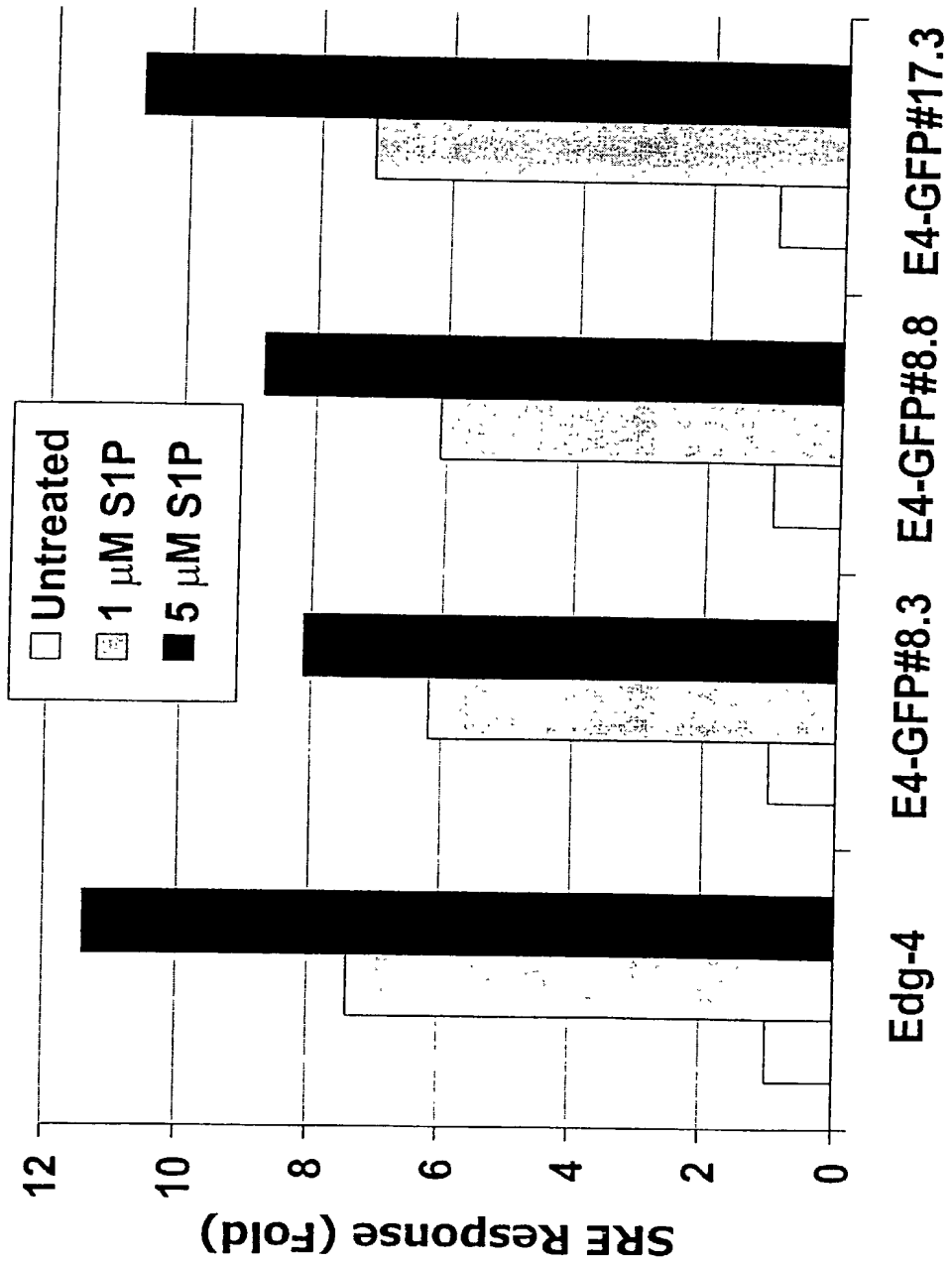


Figure 25.

